

SEQUENCE LISTING

<110> KWEE, YONG
KOSAKA, MASA AKI
KOISHIHARA, YASUO

<120> HM1.24-UTILIZING CANCER VACCINES

<130> 053466-0401

<140> 10/533,104

<141> 2005-04-28

<150> PCT/JP03/13954

<151> 2003-10-30

<150> JP 2002-316639

<151> 2002-10-30

<160> 23

<170> PatentIn Ver. 3.3

<210> 1

<211> 109

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA
comprising leader sequence and HA coding sequence

<400> 1

aattccacc atgggatgga gctgtatcat cctcttcttg gtagcaacag ctacaggtgt 60
ccactcatat ccatacgacg tccagacta cgctggtacc gcggccgcg 109

<210> 2

<211> 109

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic DNA
comprising leader sequence and HA coding sequence

<400> 2

gatccgcggc cgcggtacca gcgtagtctg ggacgtcgta tgggtatgag tggacacctg 60
tagctgttgc taccaagaag aggatgatac agtccatcc catggtggg 109

<210> 3

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 3

taaaggtacc aacagcgagg cctgccg

27

<210> 4

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 4

ctgctgcagt gagatcccag gatccata

28

<210> 5

<211> 396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(396)

<220>

<223> Nucleotide sequence of extracellular domain of soluble HM 1.24 antigenic protein

<400> 5

aac	agc	gag	gcc	tgc	cgg	gac	ggc	ctt	cgg	gca	gtg	atg	gag	tgt	cgc	48
Asn	Ser	Glu	Ala	Cys	Arg	Asp	Gly	Leu	Arg	Ala	Val	Met	Glu	Cys	Arg	
1				5				10					15			

aat	gtc	acc	cat	ctc	ctg	caa	caa	gag	ctg	acc	gag	gcc	cag	aag	ggc	96
Asn	Val	Thr	His	Leu	Leu	Gln	Gln	Glu	Leu	Thr	Glu	Ala	Gln	Lys	Gly	
			20					25					30			

ttt	cag	gat	gtg	gag	gcc	cag	gcc	gcc	acc	tgc	aac	cac	act	gtg	atg	144
Phe	Gln	Asp	Val	Glu	Ala	Gln	Ala	Ala	Thr	Cys	Asn	His	Thr	Val	Met	
			35					40					45			

gcc	cta	atg	gct	tcc	ctg	gat	gca	gag	aag	gcc	caa	gga	caa	aag	aaa	192
Ala	Leu	Met	Ala	Ser	Leu	Asp	Ala	Glu	Lys	Ala	Gln	Gly	Gln	Lys	Lys	
			50				55					60				

gtg	gag	gag	ctt	gag	gga	gag	atc	act	aca	tta	aac	cat	aag	ctt	cag	240
Val	Glu	Glu	Leu	Glu	Gly	Glu	Ile	Thr	Thr	Leu	Asn	His	Lys	Leu	Gln	
			65			70				75					80	

gac	gcg	tct	gca	gag	gtg	gag	cga	ctg	aga	aga	gaa	aac	cag	gtc	tta	288
Asp	Ala	Ser	Ala	Glu	Val	Glu	Arg	Leu	Arg	Arg	Glu	Asn	Gln	Val	Leu	
			85					90							95	

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agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc 336
Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
      100                      105                      110

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```

agc tcc gct gcg gcg ccc cag ctg ctg att gtg ctg ctg ggc ctc agc 384
Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
      115                      120                      125

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gct ctg ctg cag 396
Ala Leu Leu Gln
      130

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<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      primer

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<400> 6
ataggatcct caagcggagc tggagtcctg 30

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<210> 7
<211> 345
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)..(345)

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<220>
<223> Nucleotide sequence of extracellular domain of
      C-terminal lacking soluble HM 1.24 antigenic
      protein

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<400> 7
aac agc gag gcc tgc cgg gac ggc ctt cgg gca gtg atg gag tgt cgc 48
Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
      1           5           10           15

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aat gtc acc cat ctc ctg caa caa gag ctg acc gag gcc cag aag ggc 96
Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
      20           25           30

```

```

ttt cag gat gtg gag gcc cag gcc gcc acc tgc aac cac act gtg atg 144
Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
      35           40           45

```

```

gcc cta atg gct tcc ctg gat gca gag aag gcc caa gga caa aag aaa 192
Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
      50           55           60

```

gtg gag gag ctt gag gga gag atc act aca tta aac cat aag ctt cag 240
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 65 70 75 80

gac gcg tct gca gag gtg gag cga ctg aga aga gaa aac cag gtc tta 288
 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 85 90 95

agc gtg aga atc gcg gac aag aag tac tac ccc agc tcc cag gac tcc 336
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 100 105 110

agc tcc gct 345
 Ser Ser Ala
 115

<210> 8
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 8
 ggatcttggt tcattctcaa gcctcagaca gt 32

<210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 9
 cctcagactc ggctgaccc gtggaaagaa 30

<210> 10
 <211> 429
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide sequence coding for a fusion protein
 comprising HA peptide and soluble HM 1.24
 antigenic protein

<220>

<221> CDS

<222> (1)..(429)

<400> 10

tac	cca	tac	gac	gtc	cca	gac	tac	gct	ggg	acc	aac	agc	gag	gcc	tgc	48
Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala	Gly	Thr	Asn	Ser	Glu	Ala	Cys	
1				5				10					15			
cgg	gac	ggc	ctt	cgg	gca	gtg	atg	gag	tgt	cgc	aat	gtc	acc	cat	ctc	96
Arg	Asp	Gly	Leu	Arg	Ala	Val	Met	Glu	Cys	Arg	Asn	Val	Thr	His	Leu	
		20						25				30				
ctg	caa	caa	gag	ctg	acc	gag	gcc	cag	aag	ggc	ttt	cag	gat	gtg	gag	144
Leu	Gln	Gln	Glu	Leu	Thr	Glu	Ala	Gln	Lys	Gly	Phe	Gln	Asp	Val	Glu	
		35					40					45				
gcc	cag	gcc	gcc	acc	tgc	aac	cac	act	gtg	atg	gcc	cta	atg	gct	tcc	192
Ala	Gln	Ala	Ala	Thr	Cys	Asn	His	Thr	Val	Met	Ala	Leu	Met	Ala	Ser	
		50				55					60					
ctg	gat	gca	gag	aag	gcc	caa	gga	caa	aag	aaa	gtg	gag	gag	ctt	gag	240
Leu	Asp	Ala	Glu	Lys	Ala	Gln	Gly	Gln	Lys	Lys	Val	Glu	Glu	Leu	Glu	
65					70					75				80		
gga	gag	atc	act	aca	tta	aac	cat	aag	ctt	cag	gac	gcg	tct	gca	gag	288
Gly	Glu	Ile	Thr	Thr	Leu	Asn	His	Lys	Leu	Gln	Asp	Ala	Ser	Ala	Glu	
				85					90					95		
gtg	gag	cga	ctg	aga	aga	gaa	aac	cag	gtc	tta	agc	gtg	aga	atc	gcg	336
Val	Glu	Arg	Leu	Arg	Arg	Glu	Asn	Gln	Val	Leu	Ser	Val	Arg	Ile	Ala	
			100					105					110			
gac	aag	aag	tac	tac	ccc	agc	tcc	cag	gac	tcc	agc	tcc	gct	gcg	gcg	384
Asp	Lys	Lys	Tyr	Tyr	Pro	Ser	Ser	Gln	Asp	Ser	Ser	Ser	Ala	Ala	Ala	
		115					120					125				
ccc	cag	ctg	ctg	att	gtg	ctg	ctg	ggc	ctc	agc	gct	ctg	ctg	cag		429
Pro	Gln	Leu	Leu	Ile	Val	Leu	Leu	Gly	Leu	Ser	Ala	Leu	Leu	Gln		
		130				135					140					

<210> 11

<211> 378

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
nucleotide sequence coding for a fusion protein
comprising HA peptide and C-terminal lacking
soluble HM 1.24 antigenic protein

<220>

<221> CDS

<222> (1)..(378)

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<400> 11
tac cca tac gac gtc cca gac tac gct ggt acc aac agc gag gcc tgc 48
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
  1             5             10             15

cgg gac ggc ctt cgg gca gtg atg gag tgt cgc aat gtc acc cat ctc 96
Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
      20             25             30

ctg caa caa gag ctg acc gag gcc cag aag ggc ttt cag gat gtg gag 144
Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
      35             40             45

gcc cag gcc gcc acc tgc aac cac act gtg atg gcc cta atg gct tcc 192
Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
      50             55             60

ctg gat gca gag aag gcc caa gga caa aag aaa gtg gag gag ctt gag 240
Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
      65             70             75             80

gga gag atc act aca tta aac cat aag ctt cag gac gcg tct gca gag 288
Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu
      85             90             95

gtg gag cga ctg aga aga gaa aac cag gtc tta agc gtg aga atc gcg 336
Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala
      100            105            110

gac aag aag tac tac ccc agc tcc cag gac tcc agc tcc gct 378
Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala
      115            120            125

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<210> 12
<211> 379
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide sequence coding for L chain V region
      version a of humanized anti-HM 1.24 antibody

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<220>
<221> CDS
<222> (1)..(378)

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<220>
<221> sig_peptide
<222> (1)..(57)

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<220>
<221> mat_peptide
<222> (58)..(378)

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<400> 12
atg gga tgg agc tgt atc atc ctc tcc ttg gta gca aca gct aca ggt 48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-15 -10 -5

gtc cac tcc gac atc cag atg acc cag agc cca agc agc ctg agc gcc 96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
-1 1 5 10

agc gtg ggt gac aga gtg acc atc acc tgt aag gct agt cag gat gtg 144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
15 20 25

aat act gct gta gcc tgg tac cag cag aag cca gga aag gct cca aag 192
Asn Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
30 35 40 45

ctg ctg atc tac tcg gca tcc aac cgg tac act ggt gtg cca agc aga 240
Leu Leu Ile Tyr Ser Ala Ser Asn Arg Tyr Thr Gly Val Pro Ser Arg
50 55 60

ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc acc atc agc agc 288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

ctc cag cca gag gac atc gct acc tac tac tgc cag caa cat tat agt 336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln His Tyr Ser
80 85 90

act cca ttc acg ttc ggc caa ggg acc aag gtg gaa atc aaa c 379
Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

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<210> 13
<211> 418
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
nucleotide sequence coding for H chain V region
version r of humanized anti-HM 1.24 antibody

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<220>
<221> CDS
<222> (1)..(417)

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<220>
<221> sig_peptide
<222> (1)..(57)

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<220>
<221> mat_peptide
<222> (58)..(417)

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<400> 13
atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt 48
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
          -15                      -10                      -5

gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
          -1  1                      5                      10

cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc 144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
          15                      20                      25

act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt 192
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
          30                      35                      40                      45

gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt 240
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
          50                      55                      60

cag aag ttc aag ggc aga gtc acc atg acc gca gac aag tcc acg agc 288
Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser
          65                      70                      75

aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg 336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
          80                      85                      90

tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac 384
Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
          95                      100                      105

tgg ggg caa ggg acc acg gtc acc gtc tcc tca g 418
Trp Gly Gln Gly Thr Val Thr Val Ser Ser
110                      115                      120

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<210> 14
<211> 418
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      nucleotide sequence coding for H chain V region
      version s of humanized anti-HM 1.24 antibody

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<220>
<221> CDS
<222> (1)..(417)

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<220>
<221> sig_peptide
<222> (1)..(57)

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<220>

<221> mat_peptide

<222> (58)..(417)

<400> 14

atg gac tgg acc tgg agg gtc ttc ttc ttg ctg gct gta gct cca ggt	48
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly	
-15 -10 -5	
gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag	96
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	
-1 1 5 10	
cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc	144
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
15 20 25	
act ccc tac tgg atg cag tgg gtg cga cag gcc cct gga caa ggg ctt	192
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	
30 35 40 45	
gag tgg atg gga tct att ttt cct gga gat ggt gat act agg tac agt	240
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser	
50 55 60	
cag aag ttc aag ggc aga gtc acc atc acc gca gac aag tcc acg agc	288
Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser	
65 70 75	
aca gcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg	336
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val	
80 85 90	
tat tac tgt gcg aga gga tta cga cga ggg ggg tac tac ttt gac tac	384
Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr	
95 100 105	
tgg ggg caa ggg acc acg gtc acc gtc tcc tca g	418
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
110 115 120	

<210> 15

<211> 1014

<212> DNA

<213> Homo sapiens

<220>

<223> Nucleotide sequence coding for human HM 1.24
antigenic protein expressed on cell membrane

<220>

<221> CDS

<222> (23)..(562)

<400> 15

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gaattcggca cgagggatct gg atg gca tct act tcg tat gac tat tgc aga 52
                        Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg
                        1           5           10

gtg ccc atg gaa gac ggg gat aag cgc tgt aag ctt ctg ctg ggg ata 100
Val Pro Met Glu Asp Gly Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile
                        15           20           25

gga att ctg gtg ctc ctg atc atc gtg att ctg ggg gtg ccc ttg att 148
Gly Ile Leu Val Leu Leu Ile Ile Val Ile Leu Gly Val Pro Leu Ile
                        30           35           40

atc ttc acc atc aag gcc aac agc gag gcc tgc cgg gac ggc ctt cgg 196
Ile Phe Thr Ile Lys Ala Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg
                        45           50           55

gca gtg atg gag tgt cgc aat gtc acc cat ctc ctg caa caa gag ctg 244
Ala Val Met Glu Cys Arg Asn Val Thr His Leu Leu Gln Gln Glu Leu
                        60           65           70

acc gag gcc cag aag ggc ttt cag gat gtg gag gcc cag gcc gcc acc 292
Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu Ala Gln Ala Ala Thr
                        75           80           85           90

tgc aac cac act gtg atg gcc cta atg gct tcc ctg gat gca gag aag 340
Cys Asn His Thr Val Met Ala Leu Met Ala Ser Leu Asp Ala Glu Lys
                        95           100           105

gcc caa gga caa aag aaa gtg gag gag ctt gag gga gag atc act aca 388
Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu Gly Glu Ile Thr Thr
                        110           115           120

tta aac cat aag ctt cag gac gcg tct gca gag gtg gag cga ctg aga 436
Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu Val Glu Arg Leu Arg
                        125           130           135

aga gaa aac cag gtc tta agc gtg aga atc gcg gac aag aag tac tac 484
Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr
                        140           145           150

ccc agc tcc cag gac tcc agc tcc gct gcg gcg ccc cag ctg ctg att 532
Pro Ser Ser Gln Asp Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile
                        155           160           165           170

gtg ctg ctg ggc ctc agc gct ctg ctg cag tgagatccca ggaagctggc 582
Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
                        175           180

acatcttgga aggtccgtcc tgctcggctt ttcgcttgaa cattcccttg atctcatcag 642

ttctgagcgg gtcattggggc aacacggtta gcggggagag cacggggtag ccggagaagg 702

gcctctggag caggtctgga ggggccatgg ggcagtcctg ggtgtgggga cacagtcggg 762

ttgaccagg gctgtctccc tccagagcct ccctccggac aatgagtcce ccctcttgct 822

tcccaccctg agattgggca tgggggtgcgg tgtggggggc atgtgctgcc tgttgttatg 882

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ggttttttttt gcggggggggg ttgctttttt ctggggtctt tgagctccaa aaaaataaac 942
 acttcctttg agggagagca caccttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaattc 1002
 gggcgggccgc ca 1014

<210> 16
 <211> 132
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Amino acid sequence of soluble HM 1.24
 antigenic protein

<400> 16
 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 1 5 10 15
 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 20 25 30
 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 35 40 45
 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 50 55 60
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 65 70 75 80
 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 85 90 95
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 100 105 110
 Ser Ser Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
 115 120 125
 Ala Leu Leu Gln
 130

<210> 17
 <211> 115
 <212> PRT
 <213> Homo sapiens

<220>
 <223> Amino acid sequence of extracellular downing of
 C-terminal lacking soluble HM 1.24 antigenic
 protein

<400> 17

Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 1 5 10 15

Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 20 25 30

Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 35 40 45

Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 50 55 60

Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 65 70 75 80

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 85 90 95

Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 100 105 110

Ser Ser Ala
 115

<210> 18

<211> 143

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 amino acid sequence of a fusion protein
 comprising HA peptide and soluble HM 1.24
 antigenic protein

<400> 18

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
 1 5 10 15

Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
 20 25 30

Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
 35 40 45

Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
 50 55 60

Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
 65 70 75 80

Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu
 85 90 95

Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala
 100 105 110

Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala Ala Ala
 115 120 125

Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser Ala Leu Leu Gln
 130 135 140

<210> 19

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 amino acid sequence of a fusion protein
 comprising HA peptide and C-terminal lacking
 soluble HM 1.24 antigenic protein

<400> 19

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly Thr Asn Ser Glu Ala Cys
 1 5 10 15

Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg Asn Val Thr His Leu
 20 25 30

Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly Phe Gln Asp Val Glu
 35 40 45

Ala Gln Ala Ala Thr Cys Asn His Thr Val Met Ala Leu Met Ala Ser
 50 55 60

Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys Val Glu Glu Leu Glu
 65 70 75 80

Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln Asp Ala Ser Ala Glu
 85 90 95

Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu Ser Val Arg Ile Ala
 100 105 110

Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser Ser Ser Ala
 115 120 125

<210> 20

<211> 126

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 amino acid sequence of L chain V region
 version a of humanized anti-HM 1.24 antibody

<400> 20

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
 -15 -10 -5



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<400> 21
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
      -15                      -10                      -5

Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
      -1   1                      5                      10

Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
      15                      20                      25

Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
      30                      35                      40                      45

Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
      50                      55                      60

Gln Lys Phe Lys Gly Arg Val Thr Met Thr Ala Asp Lys Ser Thr Ser
      65                      70                      75

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
      80                      85                      90

Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
      95                      100                      105

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Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110 115 120

<210> 22
<211> 139
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
amino acid sequence of H chain V region
version s of humanized anti-HM 1.24 antibody

<400> 22
Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly
-15 -10 -5
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
-1 1 5 10
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
15 20 25
Thr Pro Tyr Trp Met Gln Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30 35 40 45
Glu Trp Met Gly Ser Ile Phe Pro Gly Asp Gly Asp Thr Arg Tyr Ser
50 55 60
Gln Lys Phe Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser
65 70 75
Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
80 85 90
Tyr Tyr Cys Ala Arg Gly Leu Arg Arg Gly Gly Tyr Tyr Phe Asp Tyr
95 100 105
Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
110 115 120

<210> 23
<211> 180
<212> PRT
<213> Homo sapiens

<220>
<223> Amino acid sequence of human HM 1.24
antigenic protein expressed on cell membrane

<400> 23
Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly
1 5 10 15
Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu
20 25 30

Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala
 35 40 45
 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg
 50 55 60
 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly
 65 70 75 80
 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met
 85 90 95
 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys
 100 105 110
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln
 115 120 125
 Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu
 130 135 140
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser
 145 150 155 160
 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser
 165 170 175
 Ala Leu Leu Gln
 180